## STIC-Biotech/ChemLib

149088

From:

Chernyshev, Olga

Sent:

Monday, March 28, 2005 3:28 PM

To:

STIC-Biotech/ChemLib

Subject:

09/826,791 sequence search request

Please search SEQ ID NO: 2 in regular and pending databases. Please print out <u>all the hits</u> down to 95% identity.

Thank you very much!

Olga N. Chernyshev, Ph.D. AU 1646 REM 3C89 2-0870 mail 4C70

STAFF USE ONLY

Type of Search

NA#:\_\_\_\_ AA#:\_Q\_\_\_(/ \x\)
Interference:\_\_\_ SPDI:\_\_\_
S/L:\_\_\_\_ Oligomer:\_\_\_\_
Encode/Transl:\_\_\_\_
Structure#:\_\_\_\_ Text:\_\_
Inventor:\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*

QUESTEL/ORBIT:\_\_\_\_\_\_
LEXIS/NEXIS:\_\_\_\_\_

SEQUENCE SYSTEM:\_\_\_\_\_\_ WWW/Internet:\_\_\_\_\_ Other(Specify):\_\_\_\_\_

## STIC-Biotech/ChemLib

147517

From: Sent:

Chernyshev, Olga Friday, March 11, 2005 9:23 AM STIC-Biotech/ChemLib

To:

Subject:

09/826,791: sequence search request

Please search SEQ ID NOS: 1, 2, 5 and 6 in regular and pending databases. Thank you very much!

Olga N. Chernyshev, Ph.D. AŬ 1646 **REM 3C89** 2-0870 mail 4C70

STAFF USE ONLY
Searcher:
Searcher Phone: 2-
Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:

Online Time:\_\_

Type of Search	
NA Sequence: #	
AA Sequence :#	
Structure: #	
Bibliographic:	
Litigation:	
Patent Family:	
Other:	

\*\*\*\*\*\*\*

Vendo	ors and cost where applicable
S	TN:
D	IALOG:
ς	UESTEL/ORBIT:
Ĺ	EXIS/NEXIS:
SE	QUENCE SYSTEM:
١	WWW/Internet:
	ther(Specify):

OM protein -

protein search, using sw model

Copyright

GenCore version (c) 1993 - 2005

5.1.6 Compugen

```
REQUENCE 2, Application US/09585876

PAtent No. 6586205

PATENT NO. 6586205

GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Immaculada
ITITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
FILE REFERENCE: 5800-88

CURRENT APPLICATION NUMBER: US/09/585,876

CURRENT FILING DATE: 2000-06-01

EARLIER APPLICATION NUMBER: 60/182,061

NUMBER OF SEQ ID NOS: 2

SOPTWARE: PASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-09-585-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 80 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                 SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo
1-09-585-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB. seq length: DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-826-791A-2
1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   April 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEPHGTFSNNNSRNCTIENF......KAKTKCVFPVSVWLRKETRV 330
                eapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2005, 11:58:33 / Search time 43 Seconds (without alignments) 572.888 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-585-876-2
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2,
```

```
밁
                            8
                                                                                                á
                                                                                                                                   멍
                                                                                                                                                                   á
                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.3
Matches 328; Conservative
317
                                301
                                                                 257
                                                                                                 241
                                                                                                                                     197
                                                                                                                                                                     181
                                                                                                                                                                                                       137
                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                          61 MINIAISDILFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
                                                                                                                                                                                                                                                                                                                                            17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
                                                                                                                                                                                                                                                                                                                                                                1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF
                                                                                                                                                       KLQTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
                                                                                                                                                                                                                        FLAMVHÞFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
                                                                                                                                                                                                                                                                          MINIAISDILFISTIPFRADYYLRGSSWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR
                                KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                                                                                                   FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
                                                                                                                                                                                                        FLAMVHPFRILHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA
KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                   FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLVLAAANACFNPLLYYFAGENFKDRL
                                                                                                                                   KLQTMNYIALVVGCULPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF
                                                                                                                                                                                                                                                                                                                                                                                                            Score 1703; DB 4;
Pred. No. 3.7e-124;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                     300
                                                                                                                                                                                                        196
                                                                                                                                       256
                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                              6
```

Search completed: April 1, 2005, 12:02:27 Job time : 43 secs